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Modeling Discrete Combinatorial Systems as Alphabetic Bipartite Networks (α -BiNs): Theory and Applications

Monojit Choudhury

Microsoft Research India, 196/36 2nd Main Sadashivnagar, 560080 Bangalore, India.

Niloy Ganguly, Abyayananda Maiti, and Animesh Mukherjee

Department of Computer Science and Engineering,
Indian Institute of Technology Kharagpur, 721302 Kharagpur, India.

Lutz Brusch and Andreas Deutsch

ZIH, TU Dresden, Zellescher Weg 12, 01069 Dresden, Germany.

Fernando Peruani*

CEA-Service de Physique de l'Etat Condensé, Centre d'Etudes de Saclay, 91191 Gif-sur-Yvette, France,
Institut des Systèmes Complexes de Paris Île-de-France, 57/59, rue Lhomond, F-75005 Paris, France.

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Life and language are *discrete combinatorial systems* (DCSs) in which the basic building blocks are finite sets of elementary units: nucleotides or codons in a DNA sequence and letters or words in a language. Different combinations of these finite units give rise to potentially infinite numbers of genes or sentences. This type of DCS can be represented as an Alphabetic Bipartite Network (α -BiN) where there are two kinds of nodes, one type represents the elementary units while the other type represents their combinations. There is an edge between a node corresponding to an elementary unit u and a node corresponding to a particular combination v if u is present in v . Naturally, the partition consisting of the nodes representing elementary units is fixed, while the other partition is allowed to grow unboundedly. Here, we extend recently analytical findings for α -BiNs derived in [Peruani et al., Europhys. Lett. **79**, 28001 (2007)] and empirically investigate two real world systems: the codon-gene network and the phoneme-language network. The evolution equations for α -BiNs under different growth rules are derived, and the corresponding degree distributions computed. It is shown that asymptotically the degree distribution of α -BiNs can be described as a family of beta distributions. The one-mode projections of the theoretical as well as the real world α -BiNs are also studied. We propose a comparison of the real world degree distributions and our theoretical predictions as a means for inferring the mechanisms underlying the growth of real world systems.

I. INTRODUCTION

Two of the greatest wonders of evolution on earth, life and language, are *discrete combinatorial systems* (DCSs) [1]. The basic building blocks of DCSs are finite sets of elementary units, such as the letters in language and nucleotides (or codons) in DNA. Different combinations of these finite elementary units give rise to a potentially infinite number of words or genes. Here, we propose a special class of complex networks as a model of DCSs. We shall refer to them as *Alphabetic Bipartite Networks* (α -BiNs) in order to signify the fact that the set of basic units, in both human and genetic languages, can be considered as an *Alphabet*.

The α -BiNs are a subclass of networks where there are two different sets (partitions) of nodes: the bipartite networks. An edge, in a bipartite network, links nodes that appear in two different partitions, but never those in the same set. In most of the bipartite networks studied in

the past both the partitions grow with time. Typical examples of this type of networks include collaboration networks such as the movie-actor [2, 3, 4, 5, 6], article-author [7, 8, 9], and board-director [10, 11] networks. In the article-author network, for instance, the articles and authors are the elements of the two partitions also known as the *ties* and *actors* respectively. An edge between an author a and an article m indicates that a has co-authored m . The authors a and a' are *collaborators* if both have coauthored the same article, i.e., if both are connected to the same node m . The concept of *collaboration* can be extended to represent, through bipartite networks, several diverse phenomena such as the city-people network [12], in which an edge between a person and a city indicates that the person has visited that particular city, the word-sentence [13, 14], bank-company [15] or donor-acceptor networks that account for injection and merging of magnetic field lines [16].

Several models have been proposed to synthesize the structure of these bipartite networks, i.e., when both the partitions grow unboundedly over time [2, 3, 4, 5, 14]. It has been found that for such growth models, when each incoming *tie* node preferentially attaches itself to

*Electronic address: fernando.peruani@iscpif.fr

the *actor* nodes, the emergent degree distribution of the *actor* nodes follows a power-law [2]. This result is reminiscent of unipartite networks where preferential attachment results in power-law degree distributions [17].

On the other hand, bipartite networks where one of the partitions remains fixed over time have received comparatively much less attention. Since the set of basic units in DCSs is always finite and constant, α -BiNs have one of its partitions fixed, the one that represents the basic units (e.g. letters, codons). In contrast, the other partition, that represents the unique discrete combinations of basic unit (e.g., words, genes), can grow unboundedly over time. Notice that the order in which the basic units are strung to form the discrete combination is an important and indispensable aspect of the system, which can be modeled within the framework of α -BiNs by allowing ordering of the edges. Nevertheless, the scope of the present work is limited to the analysis of unordered combinations. Here we assume a word to be a bag of letters and a gene a multiset of codons. Fig. 1 illustrates the concepts through the example of genes and codons.

A first systematic and analytical study of α -BiNs has been presented in [18], where a growth model for such networks based on preferential attachment coupled with a tunable randomness component has been proposed and analyzed [40]. For sequential attachment, i.e., when the edges are incorporated one by one, the exact expression for the emergent degree distribution has been derived. Nevertheless, for parallel attachment, i.e., when multiple edges are incorporated in one time step, only an approximate expression has been proposed. It has been shown that for both the cases, the degree distribution approaches a beta-distribution asymptotically with time. Depending on the value of the randomness parameter four distinct types of distributions can be observed; these, in increasing order of preferentially, are: (a) normal distribution, (b) skewed normal distribution with a single mode, (c) exponential distribution, and (d) U-shaped distribution.

In this article, we briefly review these findings and extend the analytical framework. We derive the exact growth model for parallel attachment and study the degree distribution of the one-mode projection of the network onto the alphabet nodes. These analytical findings are further applied to study two well-known DCSs from the domain of biology and language. We observe that in the codon-gene network (codons are basic units or alphabet, genes are the discrete combinations), the higher the complexity of an organism, the higher the value of the randomness parameter. Similarly, the theory can also satisfactorily explain the distribution of consonants over the languages of the world studied through the phoneme-language network (phonemes are the basic units and the sound systems of languages are the discrete combinations). Nevertheless, the study also reveals certain limitations of the current growth models. For instance, we observe that the topological characteristics of the network of co-occurrence of phonemes, which is the

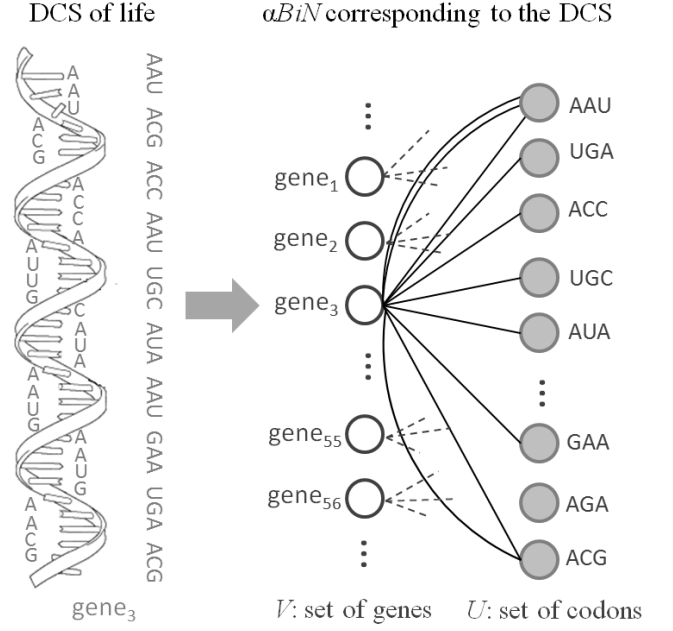


FIG. 1: DNA modeled as a bipartite network α -BiN. The set U consists of 64 codons, whereas the set V of genes is virtually infinite. Multiple occurrences of a codon in a gene have been represented here by multi-edges. For instance, the codons ‘ACG’ and ‘AAU’ have respectively 2 and 3 edges connecting to the node gene_3 . Alternatively, this could have been represented by single edges with weights 2 and 3, while the weight of the other edges would be equal to 1.

one-mode projection of the aforementioned network, is different from the theoretical predictions. This indicates that although the simple preferential attachment based growth model succeeds in explaining the degree distribution of the basic units of α -BiN, the theory fails to describe the one-mode projection, which indicates that the real dynamics of the system is much more complex.

The rest of the article is organized as follows: Sec. II formally defines α -BiN and introduces two growth models and their corresponding theoretical analysis. The two real networks – codon-gene and phoneme-language – their topology and comparison with the theoretical model are described in Sec. III A and III B respectively. In Sec. IV we summarize the obtained results, discuss the broader consequences of the present work and propose some applications and alternative perspectives on the same.

II. THEORETICAL FRAMEWORK FOR α -BINS

A. Formal definition and modeling

A bipartite graph G is a 3-tuple $\langle U, V, E \rangle$, where U and V are mutually exclusive finite sets of nodes (also known as the two partitions) and $E \subseteq U \times V$ is the set of edges

that run between these partitions. We can also define E as a multiset whose elements are drawn from $U \times V$. Clearly, this construction allows multiple edges between a pair of nodes and the number of times the nodes $u \in U$ and $v \in V$ are connected can be assumed to be the weight of the edge (u, v) . Note that although we are defining E to be a set of ordered tuples, the ordering is an implicit outcome of the fact that edges only run between nodes in U and V . In essence, we do not mean any directedness of the edges.

α -BiNs are a special type of bipartite networks where one of the partitions represents a set of basic units while the other partition represents their combinations. The set of basic units is essentially finite and fixed over time. Let us denote the unique basic units by the nodes in U . Let each unique discrete combination of the basic units be denoted as a node in V . There exists an edge between a basic unit $u \in U$ and a discrete combination $v \in V$ iff u is a part of v . If u occurs in v w times, then there are w edges between u and v , or alternatively, the weight of the edge (u, v) is w . Fig. 1 illustrates these concepts through the example of genes and codons.

Notice that the above model overlooks the order in which the basic units are strung into a particular discrete combination. The order can be taken into account by labeling the basic units in order of appearance in each element of V . However, in this work, we consider only unordered versions of DCSs. As we shall see subsequently, several real world DCSs, such as the phoneme-language network, are, in fact, unordered sets.

B. Growth model for sequential attachment

In this subsection, we review the results derived in [18] which apply to sequential as well as parallel attachment. While the results for sequential attachment are exact, for parallel attachment they represent an approximation. In the next subsection the results obtained in [18] are extended and the exact derivation for parallel attachment is presented.

The growth of α -BiNs is described in terms of a simple model based on preferential attachment coupled with a tunable randomness parameter. Suppose that the partition U has N nodes labeled as u_1 to u_N . At each time step, a new node is introduced in the set V which connects to μ nodes in U based on a predefined attachment rule. Let v_i be the node added to V during the i th time step. The theoretical analysis assumes that μ is a *constant* greater than 0. This constraint will be relaxed during synthesis of the empirical networks. However, note that if the degrees of the nodes in V are sampled from a Poisson-like distribution with mean μ , the theoretical analysis holds good asymptotically.

Let $\tilde{A}(k_i^t)$ be the probability of attaching a new edge to a node u_i , where k_i^t refers to the degree of the node u_i at time t . $\tilde{A}(k_i^t)$ defines the attachment kernel that takes

the form:

$$\tilde{A}(k_i^t) = \frac{\gamma k_i^t + 1}{\sum_{j=1}^N (\gamma k_j^t + 1)} \quad (1)$$

where the sum in the denominator runs over all the nodes in U , and γ is the tunable parameter which controls the relative weight of preferential to random attachment. Thus, the higher the value of γ , the lower the randomness in the system. Since in a bipartite network the sum of the degrees of the nodes in the two partitions are equal, the denominator in the above expression is equal to $\mu\gamma t + N$. Note that the numerator of the attachment kernel could be rewritten as $k_i^t + \alpha$, where $\alpha = 1/\gamma$ is a positive constant usually referred to as the *initial attractiveness* [19].

Physically this means that when a new discrete combination, say a gene, enters the system, it is always assumed to have μ basic units, e.g., a chain of μ codons. The patterns of the codons constituting the newly entered gene depends on the prevalence of the codons in the pre-existing genes as well as a randomness factor $1/\gamma$. At this point it is worthwhile to distinguish between a few basic sub-cases of the growth model. When $\mu = 1$, addition of a node in V is equivalent to addition of one edge in the network and thus the edges attach to the nodes in U in a sequential manner. However, for $\mu > 1$ addition of an edge is no longer a sequential process; rather μ edges are added simultaneously. We refer to the former process as *sequential attachment* and the latter as *parallel attachment*. Depending on the underlying DCS, the parallel attachment process can be further classified into two sub-cases. If it is required that the μ nodes chosen are all distinct, then we call this *parallel attachment without replacement*. On the other hand, if v_i is allowed to attach to the same node more than once, we refer to the process as *parallel attachment with replacement* [41]. Thus, parallel attachment without replacement leads to α -BiNs without multi-edges or weighted edges, while parallel attachment with replacement results in α -BiNs with multi-edges. The two cases collapse for the case of sequential attachment. To motivate the reader further, we provide some examples of natural DCSs from each of the aforementioned classes.

- *Sequential attachment*: Since in the sequential attachment model, every node in V has only one edge, it is not a discrete combination at all. Rather, each incoming v_i is a reinstantiation of some basic unit u_j . However, think of a system where U is the set of languages and V is the set of speakers, and an edge between $u \in U$ and $v \in V$ implies that u is the mother tongue of v . Although not a DCS, these type of “class and its instance” systems are plentiful in nature and can be aptly modeled using sequential attachment.
- *Parallel attachment with replacement*: Any DCS modeled as a sequence of the basic units can be thought to follow the “with replacement” model.

For instance, a gene can have many repetitions of the same codon and similarly, there may be multiple occurrences of the same word in a sentence.

- *Parallel attachment without replacement:* A DCS that is a set of the basic units can be conceived as an outcome of the “without replacement” model. For instance, the consonants and vowels (partition U) that form the repertoire of basic sounds (phonemes) of a language (partition V), proteins (U) forming protein complexes (V), etc.

In this work, we focus on the topological properties of α -BiNs that are synthesized using the sequential and parallel attachment with replacement. Nevertheless, in section III B we also present some empirical results for the parallel attachment without replacement model in the context of the phoneme-language network.

Any α -BiN has two characteristic degree distributions corresponding to its two partitions U and V . Here we assume that each node in V has degree μ and concentrate on the degree distribution of the nodes in U . Let $p_{k,t}$ be the probability that a randomly chosen node from the partition U has degree k after t time steps. We assume that initially all the nodes in U have a degree 0 and there are no nodes in V . Therefore,

$$p_{k,0} = \delta_{k,0} \quad (2)$$

Here, δ represents the Kronecker symbol. It is interesting to note that unlike the case of standard preferential attachment based growth models for unipartite (e.g., the BA model [17]) and bipartite networks (e.g., [2]), the degree distribution of the partition U in α -BiNs cannot be solved using the stationary assumption that in the limit $t \rightarrow \infty$, $p_{k,t+1} = p_{k,t}$. This is because the average degree of the nodes in U , which is $\mu t/N$, diverges with t , and consequently, the system does not have a stationary state.

In [18] it has been shown that $p_{k,t}$ can be approximated for $\mu \ll N$ and small values of γ by integrating:

$$p_{k,t+1} = (1 - A_p(k, t))p_{k,t} + A_p(k-1, t)p_{k-1,t} \quad (3)$$

where $A_p(k, t)$ is defined as

$$A_p(k, t) = \begin{cases} \frac{(\gamma k + 1)\mu}{\gamma \mu t + N} & \text{for } 0 \leq k \leq \mu t \\ 0 & \text{otherwise} \end{cases} \quad (4)$$

for $t > 0$ while for $t = 0$, $A_p(k, t) = (\mu/N)\delta_{k,0}$. The numerator contains a μ because at each time step there are μ edges that are being incorporated into the network rather than a single edge. The solution of Eq. (3) with the attachment kernel given by Eq. (4) reads:

$$p_{k,t} = \binom{t}{k} \frac{\prod_{i=0}^{k-1} (\gamma i + 1) \prod_{j=0}^{t-1-k} \left(\frac{N}{\mu} - 1 + \gamma j \right)}{\prod_{m=0}^{t-1} \left(\gamma m + \frac{N}{\mu} \right)} \quad (5)$$

As already mentioned in [18], Eq. (3) cannot describe the stochastic parallel attachment exactly because it explicitly assumes that in one time step a node of degree k

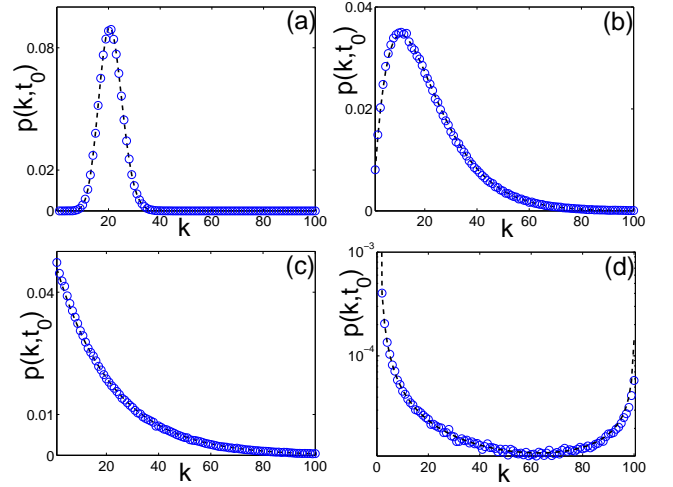


FIG. 2: The four possible degree distributions depending on γ for sequential attachment (and approximated expression for parallel attachment). Symbols represent average over 5000, in (a)-(c), and 50000, in (d), stochastic simulations. The dashed curve is the theory given by Eq. (5). From (a) to (c), $t_0 = 1000$, $N = 1000$ and $\mu = 20$. (a) at $\gamma = 0$, $p(k, t)$ becomes a binomial distribution. (b) $\gamma = 0.5$, the distribution exhibits a maximum which shifts with time for $0 \leq \gamma < 1$. (c) $\gamma = 1$, $p(k, t)$ does no longer exhibit a shifting maximum and the distribution is a monotonically decreasing function of k for $1 \leq \gamma \leq (N/\mu) - 1$. (d) $\gamma = 2500$, $t_0 = 100$, $N = 1000$ and $\mu = 1$. $p(k, t)$ becomes a u-shaped curve for $\gamma > (N/\mu) - 1$.

can only get converted to a node of degree $k + 1$. Clearly, the incorporation of μ edges in parallel allows the possibility for a node of degree k to get converted to a node of degree $k + \mu$. So, for $\mu > 1$, Eq. (5) is just an approximation of the real process for $\mu \ll N$ and small values of γ . However, for $\mu = 1$, i.e. for sequential attachment, Eq. (5) is the exact solution of the process.

Interestingly, for $\gamma > 0$, Eq. (5) approaches, asymptotically with time, a beta-distribution as follows.

$$p_{k,t} \simeq C^{-1} (k/t)^{\gamma-1} (1 - k/t)^{\eta-\gamma-1} \quad (6)$$

Here, C is the normalization constant. By making use of the properties of beta distributions, we learn that depending on the value of γ , $p_{k,t}$ can take one of the following distinctive functional forms.

- $\gamma = 0$, a binomial distribution whose mode shifts with time,
- $0 < \gamma < 1$, a skewed (normal) distribution which exhibits a mode that shifts with time,
- $1 \leq \gamma \leq (N/\mu) - 1$, a monotonically decreasing (near exponential) distribution with the mode frozen at $k = 0$, and
- $\gamma > (N/\mu) - 1$, a u-shaped distribution with peaks at $k = 0$ and $k = t$.

Fig. 2 illustrates the possible four regimes of Eq. (5). In the next subsection we present a generalization of Eq. (3) for $\mu > 1$, i.e. for parallel attachment, and solve it.

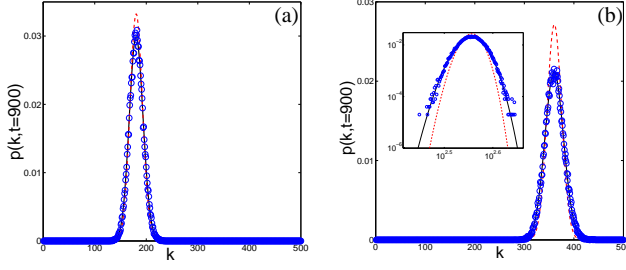


FIG. 3: Comparison for random attachment ($\gamma = 0$) between the approximation given by Eq. (5) (dashed red curve), the exact solution given by the integration of Eq. (11) (solid black curve), and stochastic simulations. Symbols correspond to average over 500 simulations. In both the figures $N = 100$. (a) corresponds to $\mu = 20$ while (b) to $\mu = 40$. The inset in (b) shows in log-log scale the deviation of the approximation with respect to the exact solution and simulations.

C. Growth model for parallel attachment with replacement

Recall that for parallel attachment, t refers to the event of introducing a new node in V with μ edges. Therefore, the correct expression for the evolution of $p_{k,t}$ has the form:

$$p_{k,t+1} = (1 - \sum_{i=1}^{\mu} \hat{A}(k, i, t)) p_{k,t} + \sum_{i=1}^{\mu} \hat{A}(k-i, i, t) p_{k-i,t} \quad (7)$$

where $\hat{A}(k, i, t)$ represents the probability at time t of a node of degree k of receiving i new edges in the next time step. The term $\sum_{i=1}^{\mu} \hat{A}(k, i, t) p_{k,t}$ describes the number of nodes of degree k at time t that change their degree due to the attachment of 1, 2, ..., or μ edges. On the other hand, nodes of degree k will be formed at time $t+1$ by the nodes of degree $k-1$ at time t that receive 1 edge, nodes of degree $k-2$ at time t that receive 2 edges, and so on. This process is described by the term $\sum_{i=1}^{\mu} \hat{A}(k-i, i, t) p_{k-i,t}$.

Next we derive an expression for $\hat{A}(k, i, t)$. We start out by a simple case: $\gamma = 0$. Since in this case the probability for an edge of attaching to a node is independent of its degree, if we add μ edges, the probability for a node of receiving a single edge is $\mu(1/N)(1-1/N)^{\mu-1}$, the probability of receiving two edges is $\binom{\mu}{2} (1/N)^2 (1-1/N)^{\mu-2}$, and for the general case we obtain the expression:

$$\hat{A}(k, i, t) = \binom{\mu}{i} \left(\frac{1}{N}\right)^i \left(1 - \frac{1}{N}\right)^{\mu-i} \quad (8)$$

To extend this result to $\gamma > 0$, we recall that if we add a single edge, the probability for a node of degree k of receiving that edge is $\phi = (\gamma k + 1) / (\mu \gamma t + N)$, where we have assumed that previous to this edge we had added μt edges to the nodes in U . Clearly, $1 - \phi$ is the probability

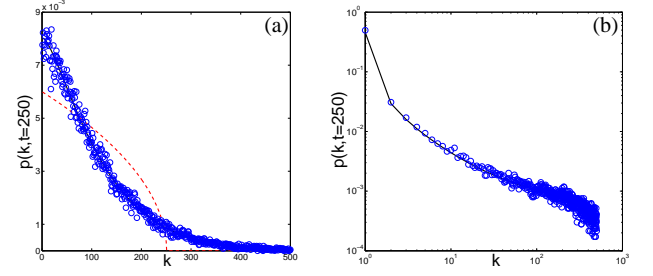


FIG. 4: Comparison for strong preferential attachment ($\gamma \geq 1$) between the approximation given by Eq. (5) (dashed red curve), the exact solution given by the integration of Eq. (11) (solid black curve), and stochastic simulations (circles), averaged over 500 runs, for parallel attachment for $\gamma \geq 1$. In both the figures $N = 100$ and $\mu = 40$. (a) corresponds to $\gamma = 1$ while (b) to $\gamma = 16$. Notice that in (b) the approximation falls out of the range of the figure, while the exact solution given by the integration of Eq. (11) describes the simulation data quite well.

for the edge to attach to some other node. Taking this into account, Eq. (8) is generalized for $\gamma \geq 0$ as

$$\hat{A}(k, i, t) = \binom{\mu}{i} \left(\frac{\gamma k + 1}{\mu \gamma t + N}\right)^i \left(1 - \frac{\gamma k + 1}{\mu \gamma t + N}\right)^{\mu-i} \quad (9)$$

Inserting expression (9) into Eq. (7), we obtain:

$$\begin{aligned} p_{k,t+1} &= \left[1 - \sum_{i=1}^{\mu} \binom{\mu}{i} \left(\frac{\gamma k + 1}{\mu \gamma t + N}\right)^i \left(1 - \frac{\gamma k + 1}{\mu \gamma t + N}\right)^{\mu-i} \right] p_{k,t} \\ &+ \sum_{i=1}^{\mu} \binom{\mu}{i} \left(\frac{\gamma(k-i) + 1}{\mu \gamma t + N}\right)^i \left(1 - \frac{\gamma(k-i) + 1}{\mu \gamma t + N}\right)^{\mu-i} p_{k-i,t} \end{aligned} \quad (10)$$

The terms between parenthesis in the first line of Eq. (10) can be simplified recalling that

$$\begin{aligned} &\left(1 - \frac{\gamma k + 1}{\mu \gamma t + N}\right)^{\mu} \\ &= 1 - \sum_{i=1}^{\mu} \binom{\mu}{i} \left(\frac{\gamma k + 1}{\mu \gamma t + N}\right)^i \left(1 - \frac{\gamma k + 1}{\mu \gamma t + N}\right)^{\mu-i} \end{aligned}$$

Therefore, Eq. (10) can be rewritten by including $i = 0$ in the sum, whereby we obtain

$$\begin{aligned} p_{k,t+1} &= \sum_{i=0}^{\mu} \binom{\mu}{i} \left(\frac{\gamma(k-i) + 1}{\mu \gamma t + N}\right)^i \\ &\quad \left(1 - \frac{\gamma(k-i) + 1}{\mu \gamma t + N}\right)^{\mu-i} p_{k-i,t} \end{aligned} \quad (11)$$

Note that Eq. (11) is a generalization of Eq. (2) in [18], which can be obtained from Eq. (11) by assigning $\mu = 1$.

In Fig. 3 we compare for random attachment ($\gamma = 0$) the approximation given by Eq. (5) (dashed red curve),

the exact solution given by the integration of Eq. (11) (solid black curve), and stochastic simulations.

Notice that the approximation, as mentioned above, deviates from the exact solution and simulations as μ increases. Looking at Fig. 3 one may wrongly conclude that the exact solution given by Eq. (11) is a very minor improvement over the approximation given by Eq. (5). However, for large values of γ (see Fig. 4), i.e., for strong preferential attachment, Eq. (5) drastically fails to describe the simulation data, while Eq. (11) accurately explains the data. To summarize, Figs. 3 and 4 validate Eq. (11) and show that, except when $\mu \ll N$ and small γ , the only way to describe the degree distribution for parallel attachment with replacement is through the integration of Eq. (11).

D. One-mode projection

In this section, we analyze the degree distribution of the one-mode projection of α -BiNs onto the set U . Formally, for an α -BiN $\langle U, V, E \rangle$, the one-mode projection onto U is a graph $G_U : \langle U, E_U \rangle$, where $u_i, u_j \in U$ are connected (i.e., $(u_i, u_j) \in E_U$) if there exists a node $v \in V$ such that $(u_i, v) \in E$ and $(u_j, v) \in E$. If there are w such nodes in V which are connected to both u_i and u_j in the α -BiN G , then there are w edges linking u_i and u_j in the one-mode projection G_U . Alternatively, one can conceive of a weighted version of G_U , where the weight of the edge (u_i, u_j) is w . In the context of the codon-gene network, the one-mode projection is a codon-codon network, where two codons are connected by as many edges as there are genes in which both of these codons occur. The one-mode projection of an α -BiN provides insight into the relationship between the basic units. For instance in linguistics the one-mode projection of the word-sentence α -BiN reveals the co-occurrence of word pairs, which in turn provides crucial information about the syntactic and semantic properties of the words (see, for example, [13, 20]).

In [21] a general technique for computing the degree distribution of the one-mode projection of a bipartite network is described. The method has been derived by making use of the concept of generating functions. As we shall see shortly, this technique is only suitable for estimating the weighted degree distribution of the one-mode projection.

Here, we propose a novel technique to derive the *thresholded degree distribution* of the one-mode projection for any arbitrary threshold. We start out by studying first the simple cases of the (non-thresholded) degree distribution of the one-mode projection for sequential and parallel attachment, to finally focus on the new technique to derive the degree distribution of the thresholded one-mode projection for parallel attachment. Notice that in order to distinguish the degree distributions of the one-mode projection from their bipartite counterpart, we shall use the symbol $p_u(k, t)$ to refer to the probability

that a randomly chosen node from the one-mode projection of an α -BiN with t nodes in V (i.e., after t time steps) has degree k .

1. Sequential attachment

Recall that in the sequential attachment based growth model only one edge is added per time step and consequently, every node in V has degree $\mu = 1$. Therefore, for any two nodes in U , say u_i and u_j , there is no node $v \in V$, which is connected to both u_i and u_j (this is because degree of v is 1). Thus, for α -BiNs that have been grown using the sequential attachment model, the one-mode projection is a degenerate graph with N nodes and 0 edges. The degree distribution of this network is

$$p_u(k, t) = \delta_{k,0} \quad (12)$$

2. Parallel attachment

Recall that in the parallel attachment model, at each time step the node which is added to V has μ edges. Consider a node $u \in U$ that has degree k in the α -BiN. Therefore, u is connected to k nodes in V , each of which is connected to $\mu - 1$ other nodes in U . Defining the degree of a node as the number of edges attached to it, in the one-mode projection, u has a degree of $q = k(\mu - 1)$. Consequently, the degree distribution of G_U , $p_u(q, t)$, is related to $p_{k,t}$ in the following way:

$$p_u(q, t) = \begin{cases} p_{0,t} & \text{if } q = 0 \\ p_{k=q/(\mu-1),t} & \text{if } \mu - 1 \text{ divides } q \\ 0 & \text{otherwise} \end{cases} \quad (13)$$

Fig. 5 shows a comparison between stochastic simulations (circles) and Eq. (13) (solid black curve). Notice that this mapping simply implies that $p_u(q = 0, t) = p_{0,t}$, $p_u(q = \mu - 1, t) = p_{1,t}$, $p_u(q = 2(\mu - 1), t) = p_{2,t}$, ..., $p_u(q = j(\mu - 1), t) = p_{j,t}$. The same result can be derived by using the generating function based technique described in Eq. 70 of [21]. It is worth noticing that q is the weighted degree of a node (i.e., the sum of the weights of all the edges incident on a node), and therefore, does not give any information about the number of distinct neighbors a node has.

3. Thresholded degree-distribution for parallel attachment

Weighted graphs, such as the one-mode projections of α -BiNs, can be converted to corresponding unweighted version by the process of *thresholding*. A thresholded one-mode projection graph (thresholded G_U) is constructed by replacing every weighted edge in G_U by a single edge iff the weight of that edge exceeds the threshold value τ ; otherwise, the edge is deleted. Thresholded degree

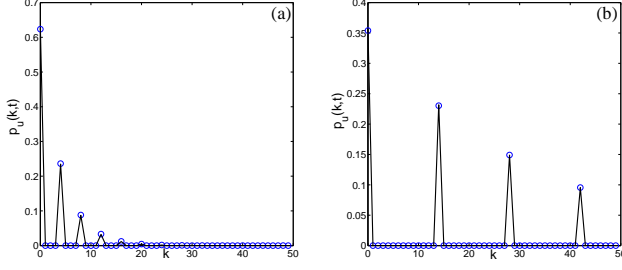


FIG. 5: Comparison between stochastic simulations for the one-mode projection (circles) and Eq. (13) (solid black curve). In both the figures $N = 500$ and $\gamma = 1$. Circles correspond to averages over 1000 simulations. In (a) $\mu = 5$ while in (b) $\mu = 15$.

distributions are more popular in the complex network literature, than their weighted counterparts (see, for example, [20, 22]). We shall denote the thresholded degree distribution at threshold τ as $p_u(q, t; \tau)$.

Let us start by considering two nodes u and u' in U with degrees k_u and $k_{u'}$, respectively. We now try to derive an expression for the probability $p(k_u, k_{u'}, m)$ that there are exactly m nodes in V that are linked simultaneously to both u and u' . In other words, $p(k_u, k_{u'}, m)$ is the probability that the number of edges running between u and u' is m , given that the degrees of the nodes are k_u and $k_{u'}$. Let us assume that the μ nodes that each node $v \in V$ is connected to, are all distinct. By the definition of the growth model for α -BiNs, the event of u being connected to a node v is independent of u' being connected to the same node. Therefore, the probability that a randomly chosen node $v \in V$ is connected to u is k_u/t and the probability that it is connected to u' is $k_{u'}/t$. Recall that t refers to the number of nodes in V . Thus, the probability that v is connected to both u and u' is $k_u k_{u'}/t^2$. Therefore, the probability that u and u' share m nodes in V takes the form:

$$p(k_u, k_{u'}, m) = \binom{t}{m} \left(\frac{k_u k_{u'}}{t^2} \right)^m \left(1 - \frac{k_u k_{u'}}{t^2} \right)^{t-m} \quad (14)$$

From Eq. (14), the probability for u and u' of sharing an edge in thresholded G_U is easily computed as:

$$p(k_u, k_{u'}; m > \tau) = \sum_{m=\tau+1}^t p(k_u, k_{u'}, m) \quad (15)$$

Consequently, in the thresholded G_U , the expected degree D of a node u whose degree is k in the α -BiN is given by:

$$D(k, \tau) = N \sum_{i=1}^t p_{i,t} p(k, i; m > \tau) \quad (16)$$

Notice that then $p_{k,t}$ can be interpreted as the probability of finding a randomly chosen node with degree $D(k, \tau)$ in

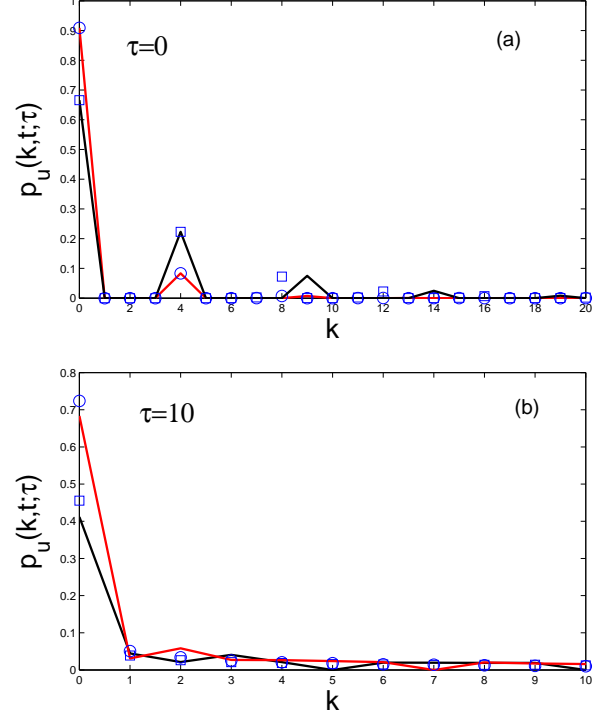


FIG. 6: Comparison between stochastic simulations for the one-mode projection at different times (symbols) and Eq. (17) (solid curve). In (a) $\tau = 0$, $N = 1000$, $\mu = 5$, $\gamma = 1$. The circles and the red curve correspond to $t = 20$, while the squares and the black curve to $t = 100$. In (b) $\tau = 10$, $N = 100$, $\mu = 20$, $\gamma = 1.5$. The circles and the red curve correspond to $t = 50$, while the squares and the black curve to $t = 100$.

the thresholded one-mode projection. Thus, the degree distribution of the thresholded G_U is computed as:

$$p_u(q, t; \tau) = \sum_{q=\lfloor D(k, \tau) \rfloor} p_k \quad (17)$$

where the function $\lfloor a \rfloor$ returns the largest integer smaller than a .

Fig. 6 shows a comparison between Eq. (17) (solid curves) and stochastic simulations (symbols) for the one-mode projection at different times. The implementation of Eq. (17) was done by summing over the $p_{k,t}$ obtained from the stochastic simulations of the corresponding α -BiN according to $q = \lfloor D(k, \tau) \rfloor$, as indicated by Eq. (16).

4. One-mode kernel

Until now we have been describing growth models for the α -BiNs. The unipartite network G_U is obtained by projecting the α -BiN onto the set of nodes U . We shall now attempt to derive a kernel for the growth of the network G_U , whereby we can construct G_U directly with-

out constructing the underlying α -BiN. Consider a node $v_t \in V$ that has been introduced in the α -BiN in the t^{th} step. There are μ nodes in U to which v_t gets connected. Let us assume that v_t is connected to no node in U more than once. This fact is true in the “parallel attachment without replacement” model that will be described in greater details in Sec. III B. However, as discussed earlier, if $\mu \ll N$ and γ is small, it is quite reasonable to make this assumption even in the case of “parallel attachment with replacement” model.

Introducing v_t in the α -BiN is equivalent to introducing a clique (complete graph) of size μ in G_U . This is because all the nodes that are connected to v_t in the α -BiN are connected to each other in G_U by virtue of sharing a common neighbor v_t . Note that this does not prohibit these μ nodes from having previous connections. The growth process is such that multiple edges, or equivalently edge weights between two nodes larger than 1 can occur.

Let us denote the degree of a node u_i in (the non-thresholded) G_U after t steps as $q_{i,t}$. As discussed in the previous subsection, $q_{i,t} = (\mu - 1)k_{i,t}$, where $k_{i,t}$ is the degree of u_i in the corresponding α -BiN after t steps. Noticing the fact that in the α -BiN the μ nodes are chosen independently of each other solely based on the attachment kernel, we can define a kernel for selecting a set of μ nodes in G_U as follows.

$$\tilde{A}(q_{a,t}, q_{b,t}, \dots) = \prod_{j=a,b,\dots} \tilde{A}(q_{j,t}/(\mu - 1)) \quad (18)$$

where a, b, \dots denotes a randomly chosen set of μ nodes in G_U . Substituting the expression provided in Eq. (1) for the preferential attachment based kernel we obtain:

$$\tilde{A}(q_{a,t}, q_{b,t}, \dots) = \prod_{j=a,b,\dots} \frac{\gamma/(\mu - 1)q_{j,t} + 1}{\sum_{i=1}^N (\gamma/(\mu - 1)q_{i,t} + 1)} \quad (19)$$

Below we summarize the growth model for the one-mode projection of the α -BiN

- Select a set of μ nodes a, b, \dots with the probability $\tilde{A}(q_{a,t-1}, q_{b,t-1}, \dots)$ as described by Eq. (19).
- Introduce edges between every pair of the chosen set a, b, \dots .
- Advance time by a unit and repeat the process.

We assume an initial condition $q_i = 0$ for all i . Alternatively, but also equivalently, the above growth model can be described as choosing μ nodes independently, each with probability $\tilde{A}(q_{i,t}/(\mu - 1))$ and then adding edges between them.

Fig. 7 plots the degree distribution obtained from the one-mode kernel and the degree distribution of the one-mode projection of the u_i nodes of the α -BiN built with the same parameters. We can see that the one-mode kernel gives quite similar degree distribution as one-mode

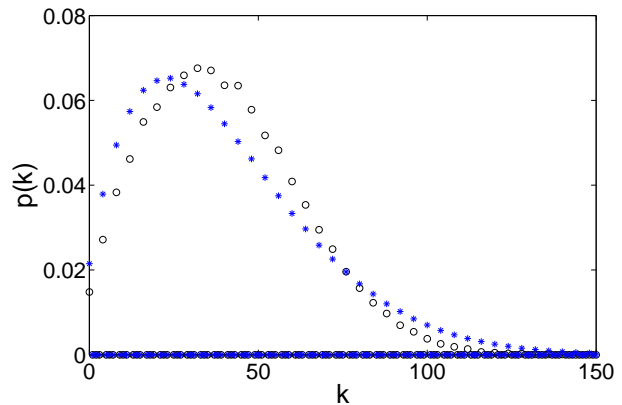


FIG. 7: Comparison between the degree distribution obtained from the stochastic simulation of Eq. (19), averaged over 1000 runs, and the one-mode projection of the α -BiN obtained using Eq. (13), averaged over 100000 runs, with $N = 50$, $\mu = 5$, $\gamma = 0.5$ at $t = 100$. Circles correspond to the one-mode kernel degree distribution, i.e., Eq. (19), while the stars are the one-mode projection of the α -BiN.

projection of the bipartite network. The primary observation from this analysis is that the kernel of the unipartite growth model has the same form as that of the bipartite growth model, with a scaling of the parameter γ by a factor of $1/(\mu - 1)$ in the former. This implies that as μ increases, the extent of degree-based preference decreases in the one-mode projection. The analysis, nevertheless is valid only for the “without replacement” model and holds approximately for the “with replacement” for $\mu \ll N$.

III. REAL WORLD α -BIN

A. CoGNet: the codon-gene network

As complete genomes of more and more organisms are sequenced, phylogenetic trees reconstructed from genomic data become increasingly detailed. Codon usage patterns in different genomes can provide insight into phylogenetic relations. However, except for some earlier work [23], studies on the codon usage have not received much attention. One of the main research issues in this context is to understand the influence of randomness in the growth pattern of genome sequences in the context of biological evolution. A well known random process in evolutionary biology is *random mutation* in a gene sequence. A gene sequence is a string defined over four symbols (A, G, T, and C) that represent the nucleotides. A *codon* is a triplet of adjacent nucleotides (eg. AGT, CTA) and codes for a specific amino acid. There are only 64 codons. Codon usage in genome sequences varies between different phylogenetic groups.

1. Definition and construction

We refer to the network of codons and genes as CoGNet and represent it as an α -BiN where V is the set of *genes*, i.e., genome of the organisms, and U is the set of nodes labeled by the codons. There is an edge $(u, v) \in E$ that run between V and U if and only if the codon u occurs in the gene v . Fig. 1 illustrates the structure of CoGNet.

We have analyzed 8 organisms belonging to widely different phylogenetic groups. These organisms have been extensively studied in biology and genetics [24] and, for our purpose importantly, their genomes have been fully sequenced. In Table I we list these organisms along with a short description and the number of genes (i.e., the cardinality of set V) and codons (i.e., the cardinality of set U). The data have been obtained from the Codon Usage Database [25, 26]. The usage of a particular codon in an organism's genome sequence can be as high as one million. In other words, the degree of the nodes in U can be arbitrarily large. This, together with the fact that there are only 64 nodes in U , presents us with the non-trivial task of estimating the probability distribution p_k , having a very large event space (between 0 and few millions), from very few observations (only 64).

A possible strategy to cope with this situation is through *binning* of the event space. For example, if we use a bin size of 10^4 , then degree 1 to degree 10^4 is compressed to a single bin which we label as 1, the next 10^4 degrees are mapped into the bin 2, and so on. Thus, if for a particular organism the codon count is m , then theoretically, the maximum degree of a codon node can be m , which in turn implies that with a bin size of 10^4 , there will be $m/10^4$ bins (or possible events) in which the 64 data points will be distributed. If all organisms are analyzed using the same bin size, depending on the length of the organism's genome, i.e., the codon count m , one obtains different number of bins. Alternatively, the bin size can be set for each organism in such a way that the resulting number of bins remains the same for all organisms. Thus, if we wish to have b bins for all organisms, the bin size for a particular organism will be m/b . Here we analyze the data using both the methods: fixed bin size and fixed number of bins.

Apart from *binning*, another way to cope with the problem of data sparseness is to compute the cumulative degree distribution $P_{k,t}$ rather than the standard degree distribution $p_{k,t}$. $P_{k,t}$ is defined as the probability that a randomly chosen node has a degree less than or equal to k . Thus,

$$P_{k,t} = \sum_{i=0}^k p_{i,t}. \quad (20)$$

The cumulative distribution is more robust to noise present in the observed data points, but at the same time it contains all the information present in $p_{k,t}$ [27]. Note that even though it is a standard practice in statistics to define cumulative distribution as stated in Eq.(20), in

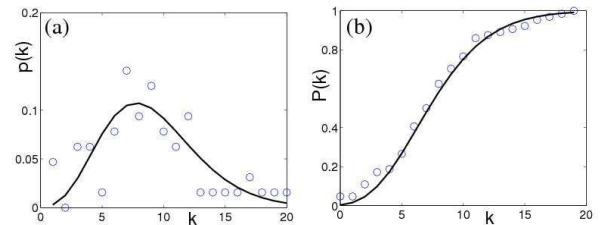


FIG. 8: Degree distribution of the codon nodes for *Xenopus leavis*. In (a) a comparison between the real data (symbols) and the theoretical $p_{k,t}$ obtained using Eq. (5) (black solid curve) is shown. The cumulative distribution of the real data (symbols) and the theory (black solid curve) is shown in (b).

complex network literature it is defined as the probability that a randomly chosen node has degree “greater than or equal to” k .

Fig.8(a) shows a comparison between the empirical degree distribution for *Xenopus leavis* (symbols) and the corresponding theoretical distribution predicted by Eq.(5) at a γ for which the squared error between the two distributions is minimum. Fig.8(b) presents the same data, but in terms of the cumulative distribution.

2. Growth model

A particular gene does not acquire all its constituent codons at a single time instance but evolves from an ancestral gene through the process of mutation (addition, deletion or substitution of codons) [28]. Therefore, we choose to apply the “sequential attachment” based growth model for synthesis of CoGNet. This means that we model the CoGNet growth through equations (3) and (5).

For all the CoGNets, the value of N is 64, μ is 1 and t corresponds to the number of codons that appears in the genome of the organism. In our model, we have a single fitting parameter, γ ; The value of γ is chosen such that the difference or error between the distributions obtained from the empirical data and the synthesized CoGNet is minimized. The error, E , is defined as follows.

$$E = \sum_{k=0}^{\infty} (p_{k,t}(\gamma) - p_{k,t}^*)^2, \quad (21)$$

where $p_{k,t}^*$ represents the empirical distribution.

Fig. 9 shows the cumulative real data and corresponding theoretical distributions of the eight organisms listed in Table I. Table. II lists the values of γ for two different methods of binning: fixed bin count (bin count = 20) fixed bin size (bin size = 10^4).

It can be observed that the values of γ get polarized into two distinct groups. The value of γ for *binning* with fixed bin size is much higher for three organisms (between 1.36 and 2.38), that are simple and primitive, than the

TABLE I: List of organisms along with their probable origin time (in Million Years Ago current time) and codon and gene counts

Organism's Name	Description	Origin time (MYA)	Gene count	Codon count
<i>Myxococcus xanthus</i>	Gram-negative rod-shaped bacterium	3200	7421	2822743
<i>Dictyostelium discoideum</i>	Soil-living amoeba	2100	3369	1962284
<i>Plasmodium falciparum</i>	Protozoan parasite	542	4098	3032432
<i>Saccharomyces cerevisiae</i>	Single-celled fungi	488	14374	6511964
<i>Xenopus laevis</i>	Amphibian, african clawed frog	416	12199	5313335
<i>Drosophila melanogaster</i>	Two-winged insect, fruit fly	270	40721	21393288
<i>Danio rerio</i>	Tropical fish, zebrafish	145	19062	8042248
<i>Homo sapiens</i>	Bipedal primates, Human	2	89533	38691091

TABLE II: The values of γ that yield best fit for the degree distribution under the two different *binning* strategies.

Organism's Name	Best γ (fixed bin size)	Best γ (fixed bin count)
<i>Myxococcus xanthus</i>	2.35	2.1
<i>Dictyostelium discoideum</i>	2.38	2.57
<i>Plasmodium falciparum</i>	1.36	1.81
<i>Saccharomyces cerevisiae</i>	0.35	0.34
<i>Xenopus laevis</i>	0.11	0.11
<i>Drosophila melanogaster</i>	0.28	0.2
<i>Danio rerio</i>	0.14	0.1
<i>Homo sapiens</i>	0.20	0.09

rest (between 0.11 and 0.35) which are more complex and came into existence at a later stage of evolution. In order to test whether bin size might influence the value of γ , the experiments were repeated with various bin sizes. The analysis reveals that the polarization of the organisms into two classes based on the value of γ is almost independent of the bin size.

We conclude that at least at the level of codon usage in *Myxococcus xanthus*, *Dictyostelium discoideum*, and *Plasmodium falciparum* the degree of randomness during codon selection is much lower than in *Saccharomyces cerevisiae*, *Xenopus laevis*, *Drosophila melanogaster*, *Danio rerio*, and *Homo sapiens*. These findings are probably correlated to the origin time and the evolutionary processes that shaped the usage of codons as follows. Let us think of evolution as the product of “copy-paste” operations. In this way, new genes emerge as result of defectuous copy-paste operations where the ancestral genes that are being copied are altered by addition, deletion or substitution of codons. Thus, copy-paste operations without defects lead to a high degree of “preferential attachment”, while mutations/defects increase the degree of randomness. In consequence, we expect newly born species/organisms to exhibit a higher degree of randomness than their ancestor, given the greater number of mutations experienced by the newly formed organisms. The value of γ in Table. II reflects this fact, and suggests that knowledge at the level of codon usage (i.e., γ) can be used as a criterion to classify organisms.

B. PlaNet: the phoneme-language network

In this section, we attempt to explain the self-organization of the consonant inventories through α -BiN where the consonants make up the basic units and languages are thought as discrete combinations of them. In fact, the most basic units of human languages are the speech sounds. The repertoire of sounds that make up the sound inventory of a language are not chosen arbitrarily. Indeed, the inventories show exceptionally regular patterns across the languages of the world, which is arguably an outcome of the self-organization that goes on in shaping their structures [29]. In order to explain this self-organizing behavior of the sound inventories, various functional principles have been proposed such as *ease of articulation* [30, 31], *maximal perceptual contrast* [30] and *learnability* [31]. The structure of vowel inventories has been successfully explained through the principle of maximal perceptual contrast [30, 31]. Although there have been some linguistically motivated work investigating the structure of the consonant inventories, most of them are limited to certain specific properties rather than providing a holistic explanation of the underlying principle of its organization.

1. Definition and construction

A first study of the consonant-language network as an α -BiN can be found in [32]. Here we follow the same definitions given in [32] and refer to the consonant-language α -BiN as PlaNet or Phoneme-Language Network. U is the universal set of consonants and V is the set of lan-

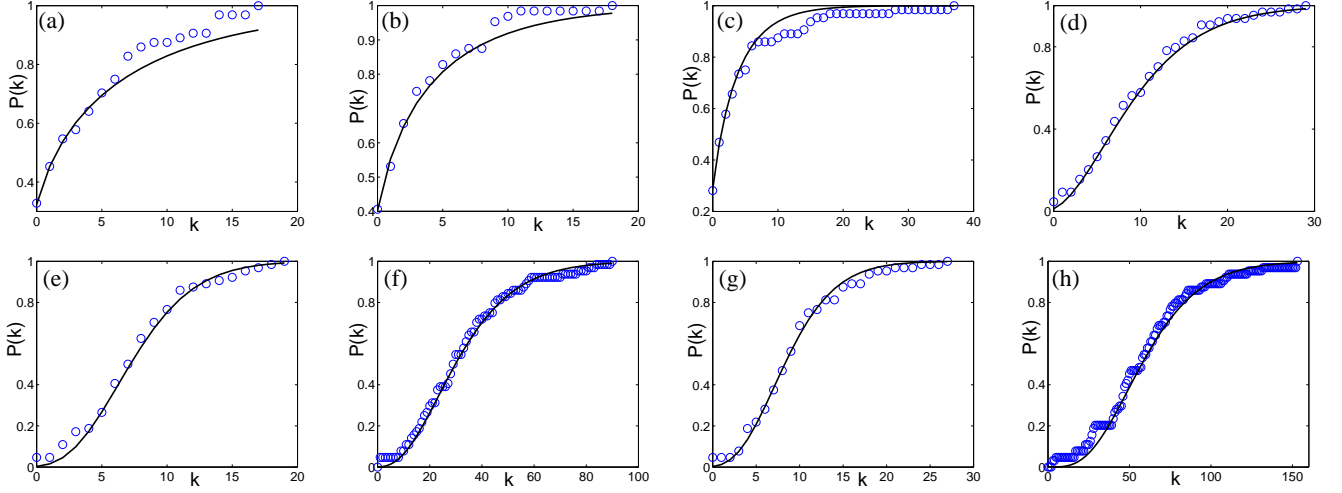


FIG. 9: Cumulative degree distributions for the empirical data (symbols) and their corresponding theoretical best γ -fits through Eqs. (3) and (5) (solid curve) for the organisms. (a) *Myxococcus xanthus*, (b) *Dictyostelium discoideum*, (c) *Plasmodium falciparum*, (d) *Saccharomyces cerevisiae*, (e) *Xenopus laevis*, (f) *Drosophila melanogaster*, (g) *Danio rerio*, and (h) *Homo sapiens*.

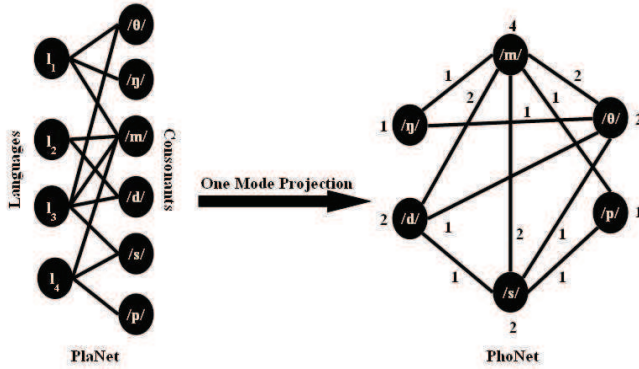


FIG. 10: Illustration of the nodes and edges of PlaNet and PhoNet.

guages of the world. There is an edge $(u, v) \in E$ iff the consonant u occurs in the sound inventory of the language v . On the other hand, the one-mode projection of PlaNet onto the consonant nodes is called PhoNet. Fig. 10 illustrates the structures of PlaNet and PhoNet. Note that PlaNet is an unweighted bipartite graph, whereas PhoNet has been represented as a weighted graph.

Many typological studies [30, 33, 34] of segmental inventories have been carried out in the past on the UCLA Phonological Segment Inventory Database (UPSID) [35]. UPSID records the sound inventories of 317 languages covering all the major language families of the world. In this work, we have used UPSID consisting of these 317 languages and 541 consonants found across them, for constructing PlaNet. Consequently, there are 317 elements (nodes) in the set V and 541 elements (nodes) in the set U . The number of elements (edges) in the set E as

computed from PlaNet and PhoNet are 7022 and 30412 respectively. We selected UPSID mainly due to two reasons – (a) it is the largest database of this type that is currently available and, (b) it has been constructed by selecting one language each from moderately distant language families, which ensures a considerable degree of “genetic” balance.

2. Topological properties

Fig. 11 illustrates the (cumulative) degree distribution of U . Since the degree of a language node is nothing but the size of the consonant inventory, we take as μ , i.e., the degree of each V node, the average number of consonants in human languages which is 22. Recall that in the theory for α -BiN the degree of each node in V has been assumed to be a constant μ .

3. Growth models

In order to obtain a theoretical description of the degree distribution of the consonant nodes in PlaNet (and later on PhoNet), we employ the α -BiN growth model described in Sec. IIB. We assume that all the language nodes have a degree $\mu = 22$. Clearly, $N = 541$ is the total number of consonant nodes and $t = 317$ is the total number of languages. Thus, γ is the only free parameter in the model. Notice that, by definition, in PlaNet a consonant can occur only once in a language inventory. Therefore, unlike the case of CoGNet, PlaNet is an α -BiN that has been constructed using a “parallel attachment without replacement” scheme. However, we expect the theory

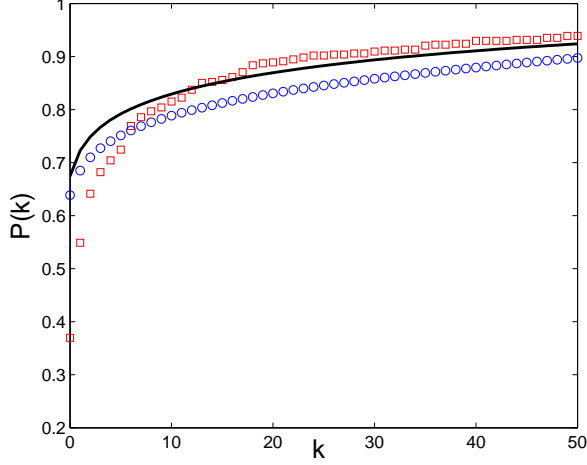


FIG. 11: Cumulative degree distribution of U , i.e., the consonant nodes. Squares correspond to the empirical data, and circles to simulations performed with “parallel attachment without replacement” with $\gamma = 14$ (PlaNet_{sim}). The solid line corresponds to the theoretical solution for “parallel attachment with replacement” (PlaNet_{theo}) obtained through integration of Eq. (10) with $\gamma = 14$.

developed in Sec. II B, corresponding to “parallel attachment with replacement”, to be a fairly good approximation for the degree distribution of PlaNet. We shall refer this theoretical model of PlaNet as PlaNet_{theo}. In order to estimate the free parameter γ , the best fit was obtained with $\gamma = 14$ (see Fig. 11). Since $1 \leq \gamma \leq N/\mu = 24.6$, based on our theoretical analysis we can conclude that the attachments are largely preferential in nature and the degrees follow a beta distribution with a single mode at $k = 1$.

To study the effect of the “parallel attachment without replacement” scheme, we carry out stochastic simulations with such a growth model described below. Suppose that a language node v_i (with degree 22) is added to the system and that $j < 22$ edges of the incoming node have already been attached to u_1, u_2, \dots, u_j distinct consonant nodes. Then, the $(j + 1)$ th edge is attached to a consonant node based on the same preferential attachment kernel (see Eq. 1), but applied on the reduced set $U - \{u_1, u_2, \dots, u_j\}$, i.e., the previously selected u_1, u_2, \dots, u_j consonant nodes cannot participate in the selection process of the $(j + 1)$ th edge of v_i . This ensures that a consonant node is never chosen twice. We shall refer to the degree distributions of the consonant nodes obtained in this way as PlaNet_{sim}. The degree distribution of PlaNet_{sim} has the best match with the degree distribution of the real PlaNet when $\gamma = 14$.

We have calculated the error for the aforementioned stochastic simulation model (E_{sim}) as well as the theory of Sec. II B, corresponding to “parallel attachment with replacement” (E_{theo}). The error has been computed us-

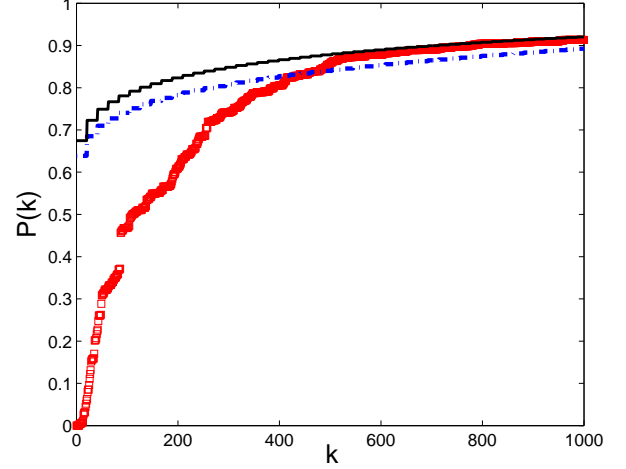


FIG. 12: Cumulative degree distribution of the one-mode projection of PlaNet (PhoNet). Squares correspond to the empirical data (Real PhoNet), dash-dotted line to simulations of one-mode projection model with “attachment without replacement” using kernel Eq. (1) (PhoNet_{sim}). The solid curve shows the theoretical degree distribution with the “attachment with replacement” scheme using Eq. (11) (PhoNet_{theo}).

ing Eq. (21) where $p_{k,t}^*$ stands for the degree distribution of the real PlaNet. It is found that $E_{sim} = 0.0972$ and $E_{theo} = 0.1170$. Since the simulation using the “parallel attachment without replacement” scheme describes the structure of consonant inventories better, the error in this case is smaller than that for “parallel attachment with replacement”.

4. One-mode projection: PhoNet

Interestingly, when we reconstruct the one-mode projection from either the theory using the “attachment with replacement” scheme (PhoNet_{theo}) or stochastic simulation considering the “attachment without replacement” model (PhoNet_{sim}), we cannot match the empirical data. Fig. 12 shows the cumulative degree distributions of PhoNet_{sim}, PhoNet_{theo} and real PhoNet. We have calculated the error of PhoNet_{sim} and PhoNet_{theo} with respect to the real PhoNet using the Eq. (21) and refer them as (E_{sim}) and (E_{theo}) respectively. Experiments reveal that $E_{sim} = 0.1230$ and $E_{theo} = 0.1438$. The results show a larger quantitative difference between the curves compared to that between their bipartite counterparts. It indicates that the one-mode projection has a more complex structure than that could have emerged from a simple preferential attachment based kernel.

Anyway, we observe that preferential attachment can explain the occurrence distribution of the consonants over languages to a good extent. One possible way to explain this observation would be that a consonant, which

is prevalent among the speakers of a given linguistic generation, tends to be more prevalent in the subsequent generations with a very little randomness involved in this whole process. It is this micro-level dynamics that manifests itself as preferential attachment in PlaNet. However, the fact that the co-occurrence distribution of the consonants, i.e., the degree distribution of PhoNet, is not explained by the growth model implies that there are other organizing principles absent in our current model that are involved in shaping the structure of the consonant inventories.

IV. DISCUSSION AND CONCLUSION

In the preceding sections, we have presented growth models for discrete combinatorial systems in the framework of a special class of networks – α -BiNs. To summarize some of our important contributions, we have

- proposed growth models for α -BiNs, which are based on preferential attachment coupled with a tunable randomness component,
- extended the mathematical analysis presented in [18] and derived the exact expression for the degree distribution in case of parallel attachment,
- analytically derived the degree distribution of the one-mode projection,
- and presented case studies for two well-known DCSs from the domain of biology and language and, thereby, we have validated our analytical findings against the empirical data.

It is worthwhile to mention here that there have been certain alternative perspectives of viewing the DCS problem presented here. One of the most celebrated among these is the “Pólya’s Urn” model (see [36]). In this classical model there is an urn initially containing r red and b blue balls. One ball is chosen randomly from the urn. The ball is then put back into the urn together with another new ball (presumably from a collection stored elsewhere) of the same color. Hence, the number of total balls in the urn grows. Generalizations of this classical model have been proposed and solved by Chung et al. in [37]. In this model, the authors assume that there are finitely many urns each containing one ball and the additional balls arrive one at a time. With each new incoming ball, a new urn is created with a probability p and the ball is placed in this newly created urn. With probability $1-p$ the ball is placed in an existing urn, where the probability that an urn, currently containing m balls, is chosen for placing the new ball is proportional to m^ν . Note that, for $p = 0$, the number of urns is fixed and finite and the model resembles the one we proposed here; however, in

this case the tunable randomness component γ , which is the most important parameter of our model, is absent. From the analysis of this model the authors find that for $\nu < 1$, the balls in all the urns grow at roughly the same rate. For $\nu > 1$, one urn dominates, i.e., the probability that any new ball goes into that urn is equal to 1. For $\nu = 1$, the fraction of balls going into each urn converges, though the limit is uniformly distributed in a certain simplex (see [37] for proofs). Here we have derived the exact analytical form for the probability distribution of the number of urns with a specified number of balls (k) after the addition of t balls. Moreover the proposed model takes into account a tunable randomness parameter, as well as the case where more than one ball are placed into the urns simultaneously (parallel attachment).

Another important issue that needs a mention is that although the reported results are strictly valid for a set of basic units fixed in time, we argue here this condition can be relaxed. We can find some real systems where the set of basic units also grow, however, at a far slower rate than the set of their discrete combinations. Under this condition we can expect the reported results to approximately hold as long as the growth rate of the basic units is slow enough.

Finally, as this study reveals, there are certain limitations of the growth models proposed here. For instance, it has been shown through simulations that the degree distribution of the consonant nodes in PlaNet is better explained by having a superlinear kernel as opposed to a linear kernel introduced here [38]. An analytical treatment of such a superlinear kernel should be an interesting topic for future research. There are also some limitations in the study of CoGNet. Selection of correct binning policy to construct the CoGNet is a challenging job. Modeling the CoGNet with parallel attachment where μ is the average number of codons present in the genes is a direct extension of the current work. As a first step, we here classified the eight organisms into two sets and we believe that our new method can further contribute to the reconstruction of phylogenetic relations. Our approach may be especially useful for the analysis of such genome sequences which are so far only available in fragments either due to fragmentary sampling of the biological material or to un-finished sequencing efforts.

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